

5' TGG CGC TTG CCG AGT GAT TCT CCT CGA ATA CCT CCT GCC GGC GCG GAG ACA CCG  
 10 19 28 37 46 55  
 GGG CGG GGG TOC TGC CGC AAC TAC CTC CCT TCC TCC TCT CCC CCG CCC CCG GAG  
 64 73 82 91 100 109  
 CCT TCA TCC TTC CCT TCC CCC CCC ACC TCG AGG GGC GGG CCT GGT TCC CGG GAC  
 118 127 136 145 154 163  
 ACC ATG TCG GAC TCT 181 190 199 208 217  
 M S D S E E E S Q D R Q L K I V V  
 CTG GGG GAC GNN GCC 235 244 253 262 271  
 L G D X A S G K T S L T T C F A Q E  
 ACT TTT GGG AAA CAG 289 298 307 316 325  
 T F G K Q Y K Q T I G L D F F L R R  
 ATA ACA TTG CCA GGA AAC 343 352 361 370 379  
 I T L P G N L N V T L CAA ATT TGG GAT ATA GGA GGG  
 388 397 406 415 424 433  
 CAG ACA ATA GGA GGC AAA ATG TTG GAT AAA TAT ATC TAT GGA GCA CAG GGA GTC  
 Q T I G G K M L D K Y I Y G A Q G V  
 CTC TTG GTA TAT GAT 451 460 469 478 487  
 L L V Y D I T N Y Q S F E N L E D W  
 TAT ACT GTG GTG AAG AAA 505 514 523 532 541  
 Y T V V K K V S X E S E T Q P L V A  
 TTG GTA GGC AAT AAA ATT 559 568 577 586 595  
 L V G N K I D L E H M R T I K P E K  
 CAC TTA CGG TTT TGC 613 622 631 640 649  
 H L R F C Q E N G F S S H F V S A K  
 ACA GGA GAC TCT GTC 667 676 685 694 703  
 T G D S V F L C F Q K V A A E I L G

FIGURE 1A

FIGURE 1B

```

      10      19      28      37      46      55
5' GCA TTG AGC CAA CAC ACA GAT TTG TCG CCT CTG TCC CCG AAG ACA CCT GCA CCC

      64      73      82      91      100      109
TCC ATG CGG ANC AAG ATG GGG AAT GGA ACT GAG GAA GAT TAT AAC TTT GTC TTC
  M  R  X  K  M  G  N  G  T  E  E  D  Y  N  F  V  F

      118      127      136      145      154      163
AAG GTG GTG CTG ATC GGC GAA TCA GGT GTG GGG AAG ACC AAT CTA CTC TCC CGA
  K  V  V  L  I  G  E  S  G  V  G  K  T  N  L  L  S  R

      172      181      190      199      208      217
TTC ACG CGC AAT GAG TTC AGC CAC GAC AGC CGC ACC ACC ATC GGG GTT GAG TTC
  F  T  R  N  E  F  S  H  D  S  R  T  I  G  V  E  F

      226      235      244      253      262      271
TCC ACC CGC ACT GTG ATG TTG GGC ACC GCT GCT GTC AAG GCT CAG ATC TGG GAC
  S  T  R  T  V  M  L  G  T  A  A  V  K  A  Q  I  W  D

      280      289      298      307      316      325
ACA GCT GGC CTG GAG CGG TAC CGA GCC ATC ACC TCG CGC TAC TAT CGT GGT GCA
  T  A  G  L  E  R  Y  R  A  I  T  S  A  Y  Y  R  G  A

      334      343      352      361      370      379
GTG GGG GCC CTC CTG GTG TTT GAC CTA ACC AAG CAC CAG ACC TAT GCT GTG GTG
  V  G  A  L  L  V  F  D  L  T  K  H  Q  T  Y  A  V  V

      388      397      406      415      424      433
GAG CGA TGG CTG AAG GAG CTC TAT GAC CAT GCT GAA GCC ACG ATC GTC GTC ATG
  E  R  W  L  K  E  L  Y  D  H  A  E  A  T  I  V  V  M

      442      451      460      469      478      487
CTC GTG GGT AAC AAA AGT GAC CTC AGC CAG GGC CGG GAA GTG CCC ACT GAG GAG
  L  V  G  N  K  S  D  L  S  Q  G  R  E  V  P  T  E  E

      496      505      514      523      532      541
GCC CGA ATG TTC GCT GAA AAC AAT GGA CTG CTC TTC CTG GAG ACC TCA GCC CTG
  A  R  M  F  A  E  N  N  G  L  L  F  L  E  T  S  A  L

      550      559      568      577      586      595
GAC TCT ACC AAT GTT GAG CTA GCC TTT GAG ACT GTC CTG AAA GAA ATC TTT GCG
  D  S  T  N  V  E  L  A  F  E  T  V  L  K  E  I  F  A

      604      613      622      631      640      649
AAG GTG TCC AAG CAG AGA CAG AAC AGC ATC CGG ACC AAT GCC ATC ACT CTG GGC
  K  V  S  K  Q  R  Q  N  S  I  R  T  N  A  I  T  L  G

      658      667      676      685      694      703
AGT GCC CAG GNT GGA CAG GAG CCT GGC CCT GGG GAG AAG AGG GCC TGT TGC ATC
  S  A  Q  X  G  Q  E  P  G  P  G  E  K  R  A  C  C  I
  
```

FIGURE 2A

		712		721		730		739		748		757					
AGC	CTC	TGA	CCT	TGG	CCA	GCA	CCA	CCT	GCC	CCC	ACT	GGC	TTT	TTG	GTG	CCC	CTT
S	L																
		766		775		784		793		802		811					
GTC	CCC	ACT	TCA	GCC	CCA	GGA	CCT	TTC	CTT	GCC	CTT	TGG	TTC	CAG	ATA	TCA	GAC
		820		829		838		847									
TGT	TCC	CTG	TTC	ACA	GCA	CCC	TCA	GGG	TCT	TAA	GGT	3'					

FIGURE 2B

5' CTG TGA TGA AAC ACT TTT CCC GTG TCG TTT GAG TGC ATC TTC TCA ACA ACC CTA  
 11 20 29 38 47 56  
 GGA GGG TTC TTG AAG CTT TTG AGA TTA ACA ATG GCA GGA AAA TCA TCA CTT TTT  
 65 74 83 92 101 110  
 AAA GTA ATT CTC CTT GGA GAT GGT GGA GTT GGG AAG AGT TCA CTT ATG AAC AGA  
 119 128 137 146 155 164  
 K V I L L G D G G V G K S S L M N R  
 TAT GTA ACT AAT AAG TTT GAT ACC CAG CTC TTC CAT ACA ATA GGT GTG GAA TTT  
 173 182 191 200 209 218  
 Y V T N K F D T Q L F H T I G V E F  
 TTA AAT AAA GAT TTG GAA GTG GAT GGA CAT TTT GTT ACC ATG CAG ATT TGG GAC  
 227 236 245 254 263 272  
 L N K D L E V D G H F V T M Q I W D  
 ACG GCA GGT CAG GAG CGA TTC CGA AGC CTG AGG ACA CCA TTT TAC AGA GGT TCT  
 281 290 299 308 317 326  
 T A G Q E R F R S L R T P F Y R G S  
 GAC TGC TGC CTG CTT ACT TTT AGT GTC GAT GAT TCA CAA AGC TTC CAG AAC TTA  
 335 344 353 362 371 380  
 D C C L L T F S V D D S Q S F Q N L  
 AGT AAC TGG AAG AAA GAA TTC ATA TAT TAT GCA GAT GTG AAA GAG CCT GAG AGC  
 389 398 407 416 425 434  
 S N W K K E F I Y Y A D V K E P E S  
 TTT CCT TTT GTG ATT CTG GGT AAC AAG ATT GAC ATA AGC GAA CGG CAG GTG TCT  
 443 452 461 470 479 488  
 F P F V I L G N K I D I S E R Q V S  
 ACA GAA GAA GCC CAA GCT TGG TGC AGG GAC AAC GGC GAC TAT CCT TAT TTT GAA  
 497 506 515 524 533 542  
 T E E A Q A W C R D N G D Y P Y F E  
 ACA AGT GCA AAA GAT GCC ACA AAT GTG GCA GCA GCC TTT GAG GAA GCG GTT CGA  
 551 560 569 578 587 596  
 T S A K D A T N V A A A F E E A V R  
 AGA GTT CTT GCT ACC GAG GAT AGG TCA GAT CAT TTT ATT CAG ACA GAC ACA GTC  
 605 614 623 632 641 650  
 R V L A T E D R S D H L I Q T D T V

FIGURE 3A

AAT	CTT	659			668		677		686		695		704
N	L	H	R	K	P	K	P	S	S	C	C		
		713			722		731		740		749		758
TGA	TGC	ATT	CTA	ACC	AAC	TCA	CAC	ATA	TAC	ACA	AAA	TCA	ACA
		767			776		785		794		803		812
AGA	GAA	TTA	GCG	TTT	GCA	GCA	GTG	TAT	CAT	CTA	CTA	ATA	AAA
		821			830		839		848		857		866
TGC	TGC	TTC	ATT	AGT	TGG	TGG	GAG	AAG	GGA	CAC	ATC	CAC	TCT
		875			884		893		902		911		920
TTT	ACT	CAA	TAA	TGG	CAC	CTT	ACA	TTT	ATA	AAT	TGT	AAC	AGT
		929			938		947		956		965		974
TTT	CTT	TAA	TTT	AAA	TAT	GTA	AGT	TGC	AGA	GCT	AAT	AAA	TGA
		983			992		1001		1010		1019		1028
TTT	AAT	TAT	AAT	AAA	AAT	AAG	AAA	CTT	GAC	TAT	TCT	AGA	AGT
		1037			1046		1055		1064		1073		1082
TTT	TCC	TGG	GAA	AAT	GGA	GAA	CTA	CTT	TTT	ATA	TGT	GTA	TGT
		1091			1100		1109		1118		1127		1136
AGC	ATT	GTA	TTC	TTG	GTT	CAG	GGA	AAT	ACT	TTC	CTA	AAG	CAA
		1145			1154		1163		1172				
TTA	AAG	ATT	AAA	ATC	TAA	TGT	AAA	AAA	AAA	AAA	AAA	AAA	3'

FIGURE 3B

1 M S D S E E E E S Q D R Q - - - - L K I V V L G D X A S G K T SEQ ID NO-1  
 1 M S D S E E E E S Q D R Q - - - - L K I V V L G D G T S G K T GI 1154901  
 1 M R K K M G N G T E E D Y N F V F K V V L T G E S G V G K T SEQ ID NO-3  
 1 M G N - - - - G K E E D Y N F V F K V V L I G E S G V G K T GI 436001  
 1 M A G K S S - - - - - L F K V I L L G D G G V G K S SEQ ID NO-5  
 1 M A G K S S - - - - - L F K V I L L G D G G V G K S GI 486830

27 S L T T C F A Q E T F G K Q Y K Q T I G L D F F L R R I T L SEQ ID NO-1  
 27 S L A T C F A Q E T F G K Q Y K Q T I G L D F F L R R I T L GI 1154901  
 31 N L L S R F T R N E F S H D S R T T I G V E F S T R T V M L SEQ ID NO-3  
 27 N L L S R F T R N E F S H D S R T T I G V E F S T R T V L L GI 436001  
 22 S L M N R Y V T N K F D T Q L F H T I G V E F L N K D L E V SEQ ID NO-5  
 22 S L M N R Y V T N K F D T Q L F H T I G V E F L N K D L E V GI 486830

57 P G N L N V T L Q I W D I G G Q T I G G K M L D K Y I Y G A SEQ ID NO-1  
 57 P G N L N V T L Q I W D I G G Q T I G G K M L D K Y I Y G A GI 1154901  
 61 G T A A - - V K A Q I W D T A G L E R Y R A I T S A Y Y R G A SEQ ID NO-3  
 57 G T A A - - V K A Q I W D T A G L E R Y R A I T S A Y Y R G A GI 436001  
 52 D G H F - - V T M Q I W D T A G Q E R F R S L R T P F Y R G S SEQ ID NO-5  
 52 D G H F - - V T M Q I W D T A G Q E R F R S L R T P F Y R G S GI 486830

87 Q G V L L V Y D I T N Y Q S F E N L E D W Y S V V V K K V S X SEQ ID NO-1  
 87 Q G I L L V Y D I T N Y Q S F E N L E D W Y S V V V K K V S X GI 1154901  
 90 V G A L L V F D L T K K H Q T Y A V V E R W L K E L - - Y D H SEQ ID NO-3  
 86 V G A L L V F D L T K K H Q T Y A V V E R W L K E L - - Y D H GI 436001  
 81 D C C L L T F S V D D S Q S F Q N L S N W K K E F I Y Y A D SEQ ID NO-5  
 81 D C C L L T F S V D D S Q S F Q N L S N W K K E F I Y Y A D GI 486830

117 E S E T Q P L V - A L V G N K I D L E H M R T I K P E K H L SEQ ID NO-1  
 117 E S E T Q P L V - A L V G N K I D L E H M R T I K P E K H L GI 1154901  
 118 A E A - - T I V V M L V G N K K S D L S Q G R E V P T E E A R SEQ ID NO-3  
 114 A E A - - T I V V M L V G N K K S D L S Q A R E V P T E E A R GI 436001  
 111 V K E P E S F P F V I L G N K I D I S E - R Q V S T E E A Q SEQ ID NO-5  
 111 V K E P E S F P F V I L G N K I D I S E - R Q V S T E E A Q GI 486830

146 R F C Q E N G F S S H F - V S A K T G D S V F L C F Q K V A SEQ ID NO-1  
 146 R F C Q E N G F S S H F - V S A K T G D S V F L C F Q K V A GI 1154901  
 146 M F A E N N G - L L F L E T S A L D S T N V E L A F E T V L SEQ ID NO-3  
 142 M F A E N N G - L L F L E T S A L D S T N V E L A F E T V L GI 436001  
 140 A W C R D N G D Y P Y F E T S A K D A T N V A A A F E E A V SEQ ID NO-5  
 140 A W C R D N G D Y P Y F E T S A K D A T N V A A A F E E A V GI 486830

175 A E I L G I K L N X X Q X X S H X G V V K X X I V N Y N Q SEQ ID NO-1  
 175 A E I L G I K L N K A E I E Q S Q R - V V K A D I V N Y N Q GI 1154901  
 175 K E I F - - - - - A K V S K Q R Q N S T R T N A I T L G S SEQ ID NO-3  
 171 K E I F - - - - - A K V S K Q I Q N S P R S N A I A L G S GI 436001  
 170 R R V L - - - - - A T - E D R S D H L I Q T D T V N L - - SEQ ID NO-5  
 170 R R V L - - - - - A T - E D R S D H L I Q T D T V S L - - GI 486830

205 E P M S R T X N P P R S S M C A V Q SEQ ID NO-1  
 204 E P M S R T V N P P R S S M C A V Q GI 1154901  
 199 A Q X G Q E P G P G K R A C C I S L SEQ ID NO-3  
 195 A Q A G Q E P G P G Q K R A C C I N L GI 436001  
 191 - - - - - H R K P K P S S S C C SEQ ID NO-5  
 191 - - - - - H R K P K P S S S C C GI 486830

FIGURE 4

0988974-111901

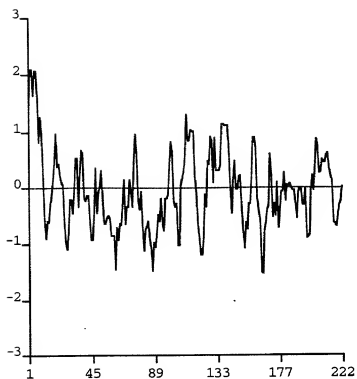


FIGURE 5



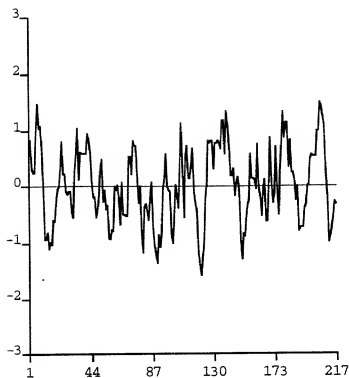


FIGURE 6

09988974-111901

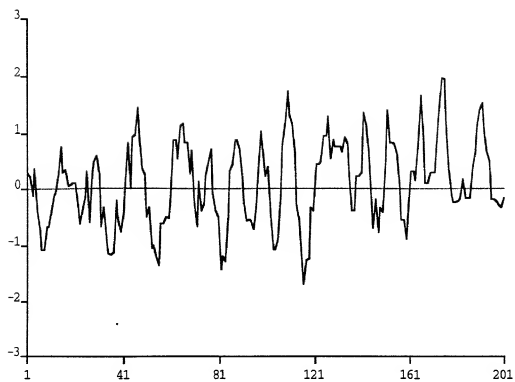


FIGURE 7

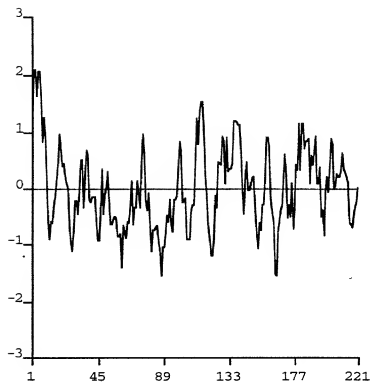


FIGURE 8